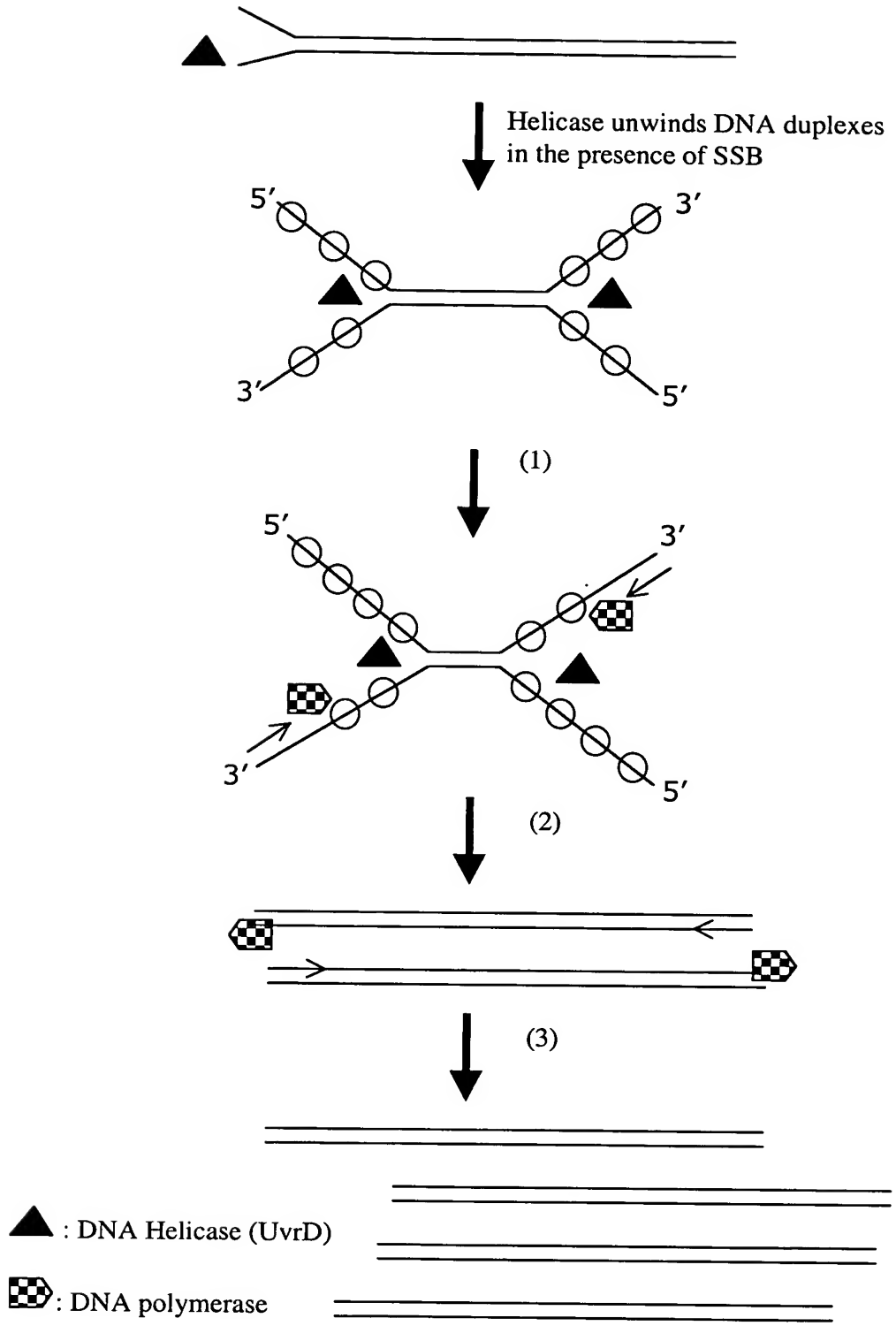
Helicase unwinds DNA duplexes
in the presence of SSB
5′
3′
3′
5′
(1)
5′
3′
3′
5′
(2)
(3)
: DNA Helicase (UvrD)
: DNA polymerase
: Single-stranded DNA
binding protein (SSB)

Figure 1.

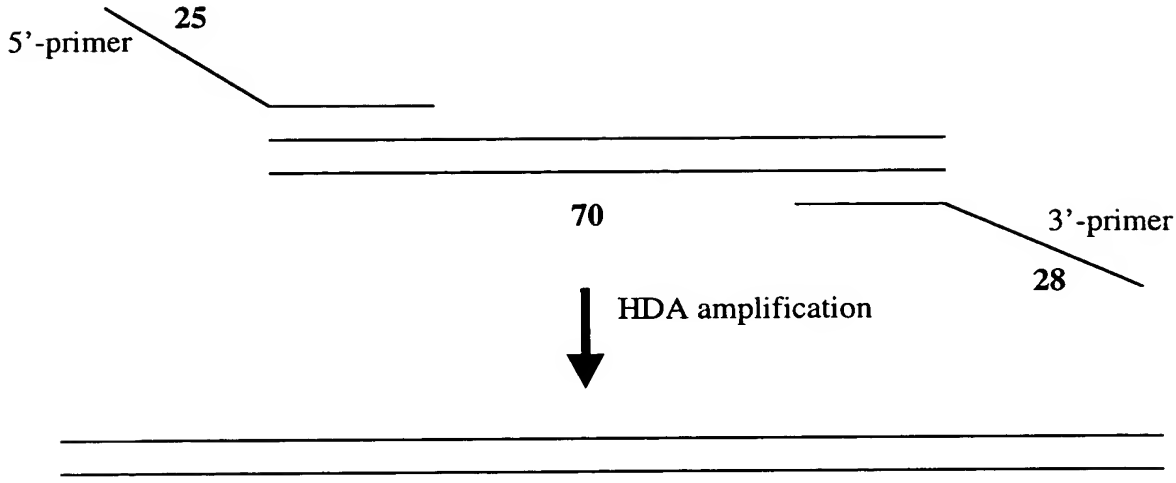

Figure 2A

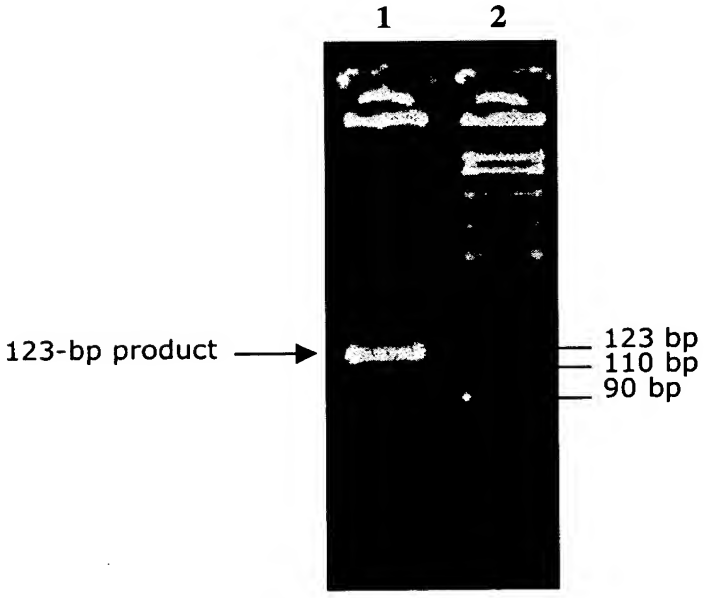

Figure 2B.

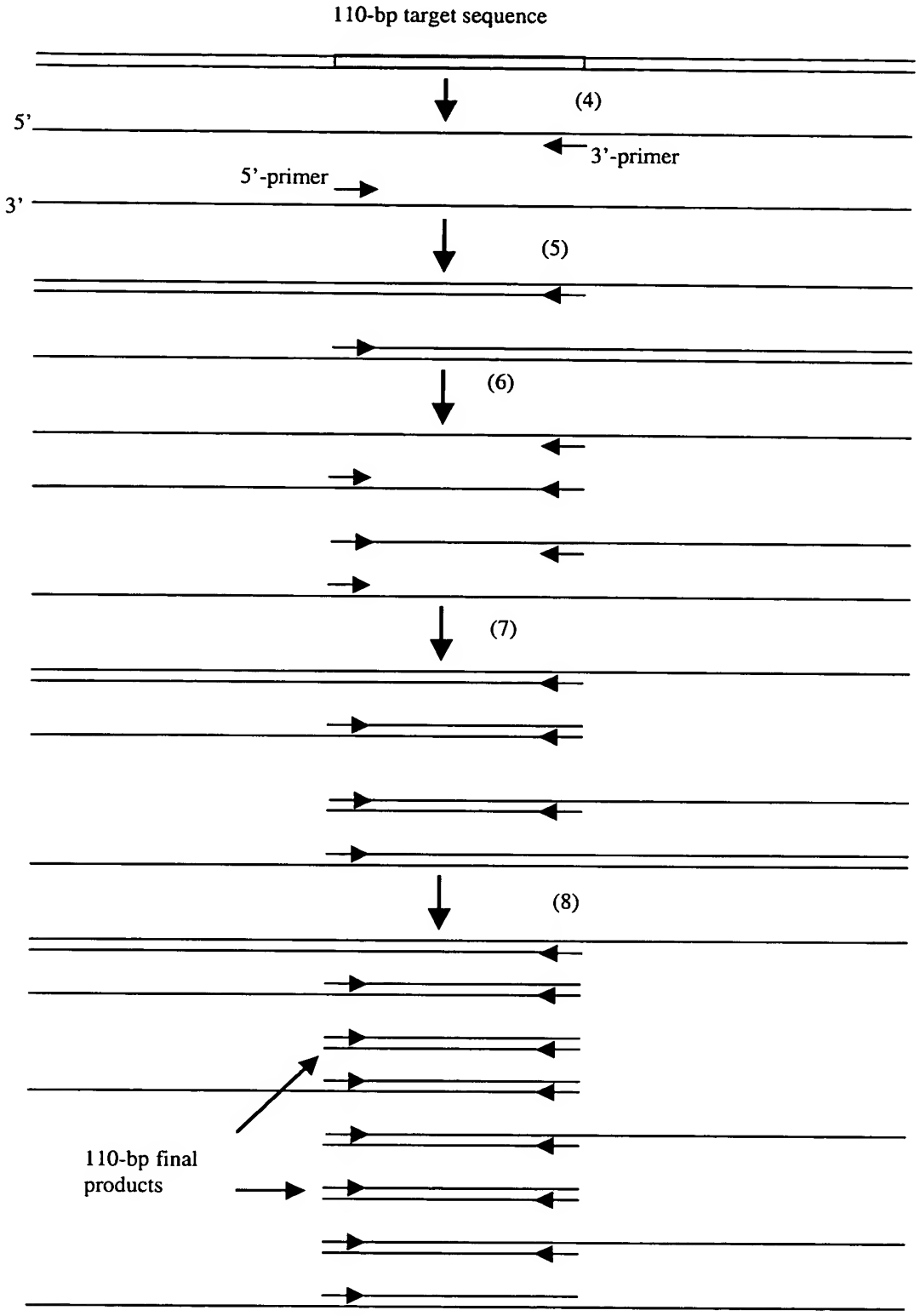
110-bp target sequence
(4)
5'
3'-primer
5'-primer
3'
(5)
(6)
(7)
(8)
110-bp final
products

Figure 3

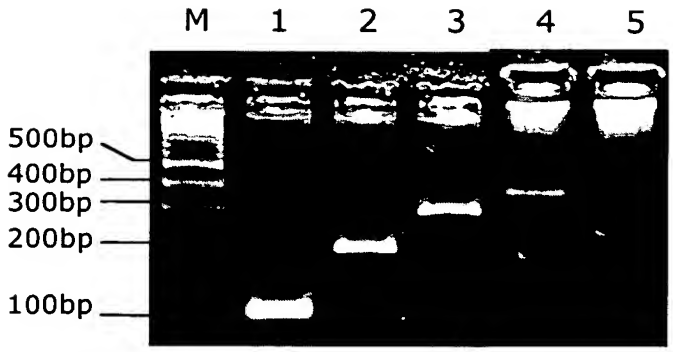

Figure 4

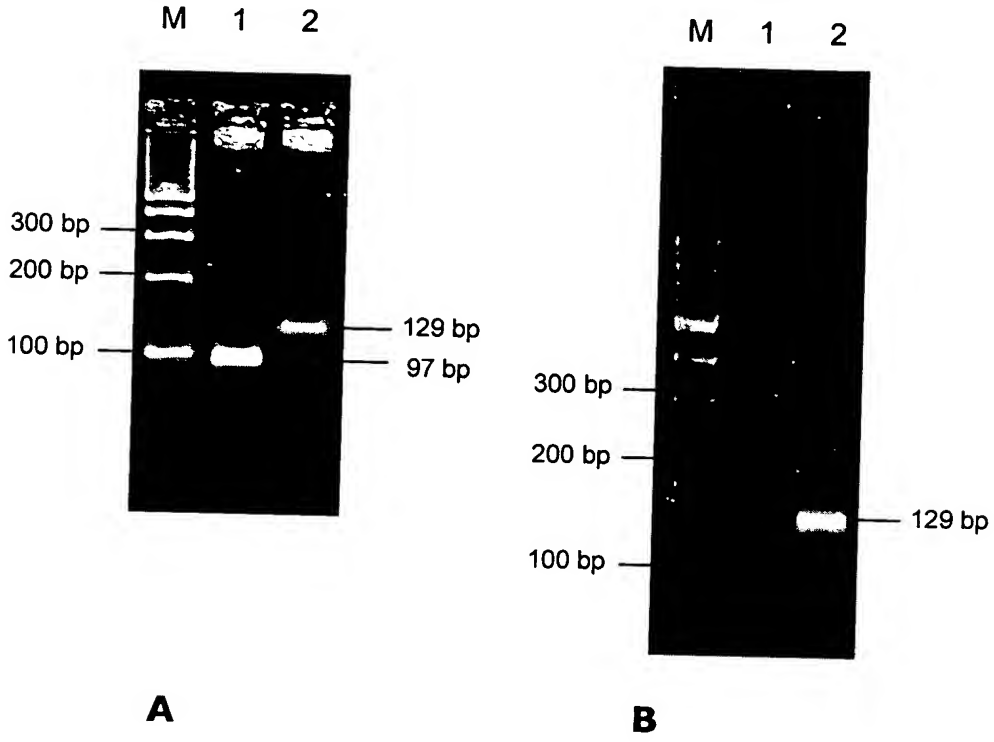
M
1
2
300 bp
200 bp
100 bp
129 bp
97 bp
A
M
1
2
300 bp
200 bp
100 bp
129 bp
B

Figure 5

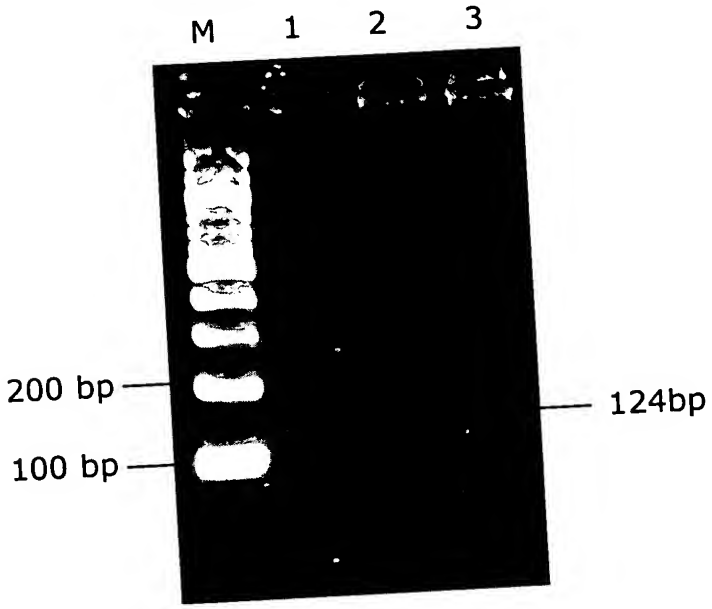

Figure 6

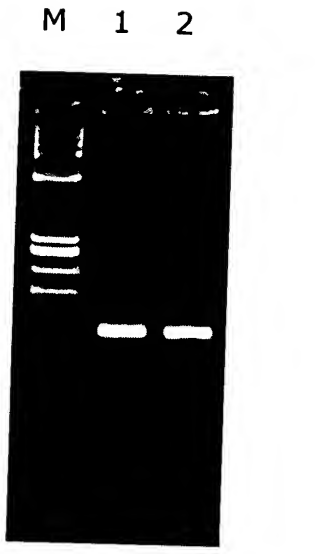

Figure 7

Genome Copies 10^7 10^6 10^5 10^4 10^3 10^2 10 0

Figure 8

Figure 9

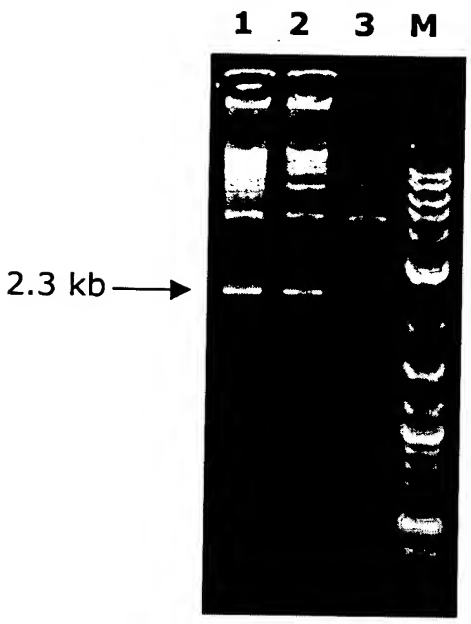

Figure 10

Figure 11

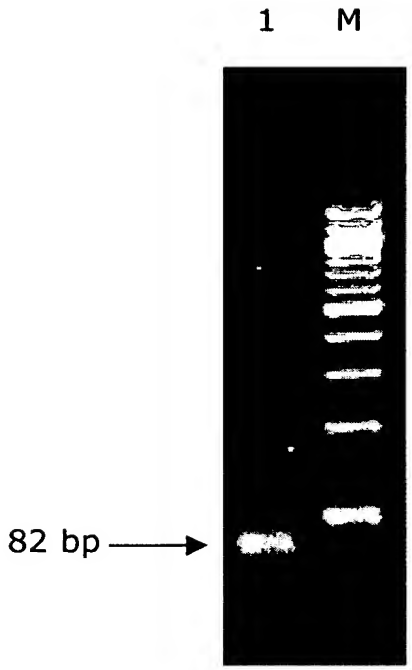

Figure 12

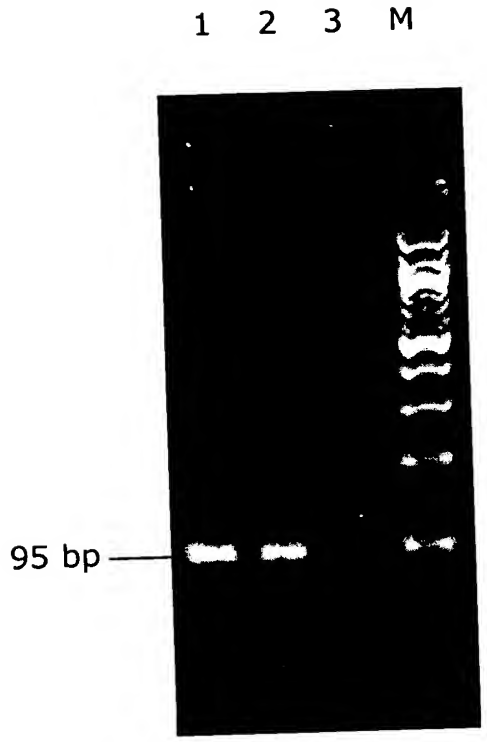

Figure 13

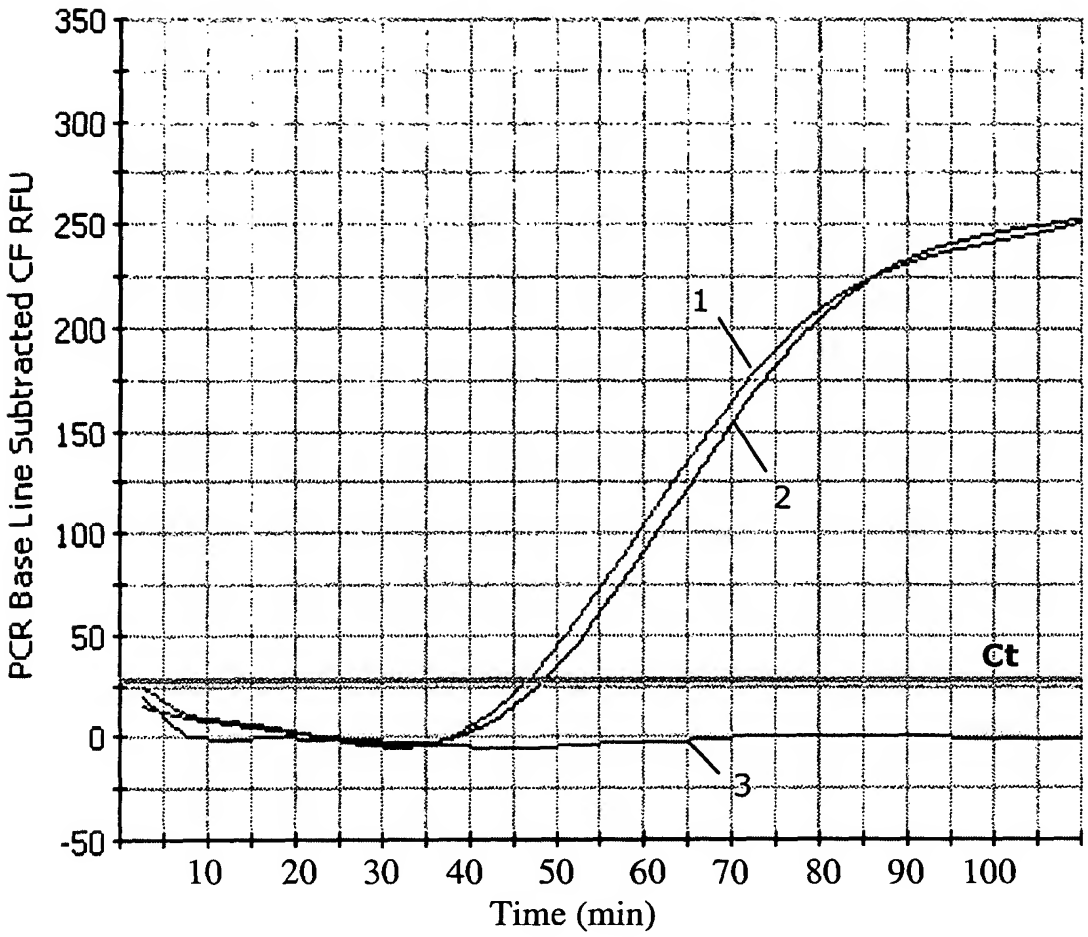
PCR Base Line Subtracted CF RFU
350
300
250
200
150
100
50
0
-50
10
20
30
40
50
60
70
80
90
100
Time (min)
1
2
3
Ct

Figure 14

FIGURE 15-1

TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACA
TGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCG
GATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGC
GGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGG
CATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT
GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGC
ATCAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTGG
GAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCA
GCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTT
GGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA
CGACGGCCAGTGAATTGCATGCTCAGCTTGGCGTAATCA
TGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCA
CAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTA
AAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAA
TTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACC
TGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCG
GGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTC
CTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCG
GCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGT
TATCCACAGAATCAGGGGATAACGCAGGAAAGAACATG
TGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAA
GGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCC
TGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT
GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTT
CCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC
CTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCG
GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT
CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGT
GTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTA
TCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAC
GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT
AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTT
GAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAG
TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG
GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCA

FIGURE 15-2

CCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGA
TTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGA
TCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACT
CACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGA
TCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAA
ATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAG
TTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGAT
CTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTC
GTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGC
CCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACC
GGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAG
GGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTC
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAG
TAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCAT
TGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTAT
GGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT
TACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTC
CTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGC
AGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTC
TCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACT
GGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATG
CGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGA
TAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCAT
CATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGAT
CTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCG
TGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGC
GTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGC
AAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATAC
TCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCA
GGGTTATTGTCTCATGAGCGGATACATATTTGAATGTAT
TTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCC
CCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTAT

FIGURE 15-3

CATGACATTAACCTATAAAAATAGGCGTATCACGAGGCC
CTTTCGTC

FIGURE 16

ATGAGTAGGCGTGAAGTAAAAAATCAAACAAATATTTCT
AGAATTGAAGGAATTAAACCAAATGATGCTTATGTTGCT
TATGTATGTGTACAATGTAACAATTTGAATATGATAAATA
TTGGACAAAAATTATTAGATCCAAGAGAGGCTTATGAAA
CACAAGAATGGAAATGTGAAAGATGTGGATTTTTACATA
GTAAAAATAATTCATTGTCTTATTCAAACTGGCCAGAAG
AAAGTAAAAAGAAAGGTTCTATTCCTGTACAAAGATTTT
GGCAAGCTTTTTTTAGAGTATATACAGAGAATAAAGAAG
CATATTGGAAACAATGTAATTGTTGTGGAAAAATATTAC
CATTTTCCGCATTTAGCAAGCATATTGGTTTTGGCCCTCT
TGAAAGACAAATGGAATGTAGAGCTTGTAAGGGAGTGA
TAAATGCATTTTTAAATCCAGAAAGAACAGAAGATCAAT
TAAGAGAGTCAAATGTTAGGAGACGTGTTGCCGATTTGT
TTGTTAAAAAAGAAAATAAATCTAAAGATGATGGATTTAT
TAAAGATTTATTTAAACGTTTTGGTTCAAAGTGCTTTAAA
ACAAAGAAATATCTAAATATTCATGATAGAAATTCTTGG
GCTATAGATCATATTTTACCATCAAAATATCTTTATCCTC
TTACAAAAGAAAATGCTGCACTATTATCTGTAGAAGCTA
ATTCCAATAAAAGAGATCGTTGGCCTTCAGAATTTTATAC
AAATAATGAATTAATAGAACTTGCTACAATAACAGGAGC
TGATTTACAATTATTATCAAATAAAACACCTATTATAAAT
CCAAATCTTACTGATGAGGATATAAATGCAGGTATTGAG
AATTATTTGTCTGTTCGTGAAAATTCAAACCTTGAGAAGC
GAGTAGCTGAAATAAAAAAAATCATAATAGACTATCAAT
TAACGGATAAATTATCGAAAAGCAACAAGAATTTACTTG
GTTTATCTTAA